

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: De Robertis, Edward M.
Bouwmeester, Tewis
- (ii) TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing Factors
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Majestic, Parsons, Siebert & Hsue
 - (B) STREET: Four Embarcadero Center, Suite 1100
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 94111-4106
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/878,474
 - (B) FILING DATE: 18-JUN-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/020,150
 - (B) FILING DATE: 20-JUN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Siebert, J. Suzanne
 - (B) REGISTRATION NUMBER: 28,758
 - (C) REFERENCE/DOCKET NUMBER: 3100.002US1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415/248-5500
 - (B) TELEFAX: 415/362-5418

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Leu	Leu	Asn	Val	Leu	Arg	Ile	Cys	Ile	Ile	Val	Cys	Leu	Val	Asn	
1				5					10					15		
Asp	Gly	Ala	Gly	Lys	His	Ser	Glu	Gly	Arg	Glu	Arg	Thr	Lys	Thr	Tyr	
			20					25					30			
Ser	Leu	Asn	Ser	Arg	Gly	Tyr	Phe	Arg	Lys	Glu	Arg	Gly	Ala	Arg	Arg	
		35					40					45				
Ser	Lys	Ile	Leu	Leu	Val	Asn	Thr	Lys	Gly	Leu	Asp	Glu	Pro	His	Ile	
	50					55					60					
Gly	His	Gly	Asp	Phe	Gly	Leu	Val	Ala	Glu	Leu	Phe	Asp	Ser	Thr	Arg	
65					70					75					80	
Thr	His	Thr	Asn	Arg	Lys	Glu	Pro	Asp	Met	Asn	Lys	Val	Lys	Leu	Phe	
				85					90					95		
Ser	Thr	Val	Ala	His	Gly	Asn	Lys	Ser	Ala	Arg	Arg	Lys	Ala	Tyr	Asn	
			100					105					110			
Gly	Ser	Arg	Arg	Asn	Ile	Phe	Ser	Arg	Arg	Ser	Phe	Asp	Lys	Arg	Asn	
		115					120					125				
Thr	Glu	Val	Thr	Glu	Lys	Pro	Gly	Ala	Lys	Met	Phe	Trp	Asn	Asn	Phe	
	130					135					140					
Leu	Val	Lys	Met	Asn	Gly	Ala	Pro	Gln	Asn	Thr	Ser	His	Gly	Ser	Lys	
145					150					155					160	
Ala	Gln	Glu	Ile	Met	Lys	Glu	Ala	Cys	Lys	Thr	Leu	Pro	Phe	Thr	Gln	
				165					170					175		
Asn	Ile	Val	His	Glu	Asn	Cys	Asp	Arg	Met	Val	Ile	Gln	Asn	Asn	Leu	
			180					185					190			
Cys	Phe	Gly	Lys	Cys	Ile	Ser	Leu	His	Val	Pro	Asn	Gln	Gln	Asp	Arg	
	195						200					205				
Arg	Asn	Thr	Cys	Ser	His	Cys	Leu	Pro	Ser	Lys	Phe	Thr	Leu	Asn	His	
	210					215					220					

Leu	Thr	Leu	Asn	Cys	Thr	Gly	Ser	Lys	Asn	Val	Val	Lys	Val	Val	Met
225					230					235					240
Met	Val	Glu	Glu	Cys	Thr	Cys	Glu	Ala	His	Lys	Ser	Asn	Phe	His	Gln
				245					250					255	
Thr	Ala	Gln	Phe	Asn	Met	Asp	Thr	Ser	Thr	Thr	Leu	His	His		
			260					265				270			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCCTAA AAGCGGCACA GTGCAGGAAC AGCAAGTCGC TCAGAAACAC TGCAGGGTCT	60
AGATATCATA CAATGTTACT AAATGTACTC AGGATCTGTA TTATCGTCTG CCTTGTGAAT	120
GATGGAGCAG GAAAACACTC AGAAGGACGA GAAAGGACAA AAACATATTC ACTTAACAGC	180
AGAGGTTACT TCAGAAAAGA AAGAGGAGCA CGTAGGAGCA AGATTCTGCT GGTGAATACT	240
AAAGGTCTTG ATGAACCCCA CATTGGGCAT GGTGATTTTG GCTTAGTAGC TGAACTATTT	300
GATTCCACCA GAACACATAC AAACAGAAAA GAGCCAGACA TGAACAAAGT CAAGCTTTTC	360
TCAACAGTTG CCCATGGAAA CAAAAGTGCA AGAAGAAAAG CTTACAATGG TTCTAGAAGG	420
AATATTTTTT CTCGCCGTTT TTTTGATAAA AGAAATACAG AGGTTACTGA AAAGCCTGGT	480
GCCAAGATGT TCTGGAACAA TTTTTTGGTT AAAATGAATG GAGCCCCACA GAATACAAGC	540
CATGGCAGTA AAGCACAGGA AATAATGAAA GAAGCTTGCA AAACCTTGCC CTTCACTCAG	600
AATATTGTAC ATGAAACTG TGACAGGATG GTGATACAGA ACAATCTGTG CTTTGGTAAA	660
TGCATCTCTC TCCATGTTCC AAATCAGCAA GATCGACGAA ATACTTGTTT CCATTGCTTG	720
CCGTCCAAAT TTACCCTGAA CCACCTGACG CTGAATTGTA CTGGATCTAA GAATGTAGTA	780
AAGGTTGTCA TGATGGTAGA GGAATGCACG TGTGAAGCTC ATAAGAGCAA CTTCCACCAA	840

ACTGCACAGT TTAACATGGA TACATCTACT ACCCTGCACC ATTAAAAGGA CTGTCTGCCA 900
 TACAGTATGG AAATGCCCAT TTGTTGGAAT ATTCGTTACA TGCTATGTAT CTAAAGCATT 960
 ATGTTGCCTT CTGTTTCATA TAACCACATG GAATAAGGAT TGTATGAATT ATAATTAACA 1020
 AATGGCATT TGTGTAACAT GCAAGATCTC TGTTCCATCA GTTGCAAGAT AAAAGGCAAT 1080
 ATTTGTTTGA CTTTTTCTA CAAAATGAAT ACCCAAATAT ATGATAAGAT AATGGGGTCA 1140
 AAAGTGTAA GGGGTAATGT AATAATAGGG ACTAACAACC AATCAGCAGG TATGATTTAC 1200
 TGGTCACCTG TTAAAAGCA AACATCTTAT TGGTTGCTAT GGGTTACTGC TTCTGGGCAA 1260
 AATGTGTGCC TCATAGGGGG GTTAGTGTGT TGTGTACTGA ATTAATTGTA TTTATTTTCA 1320
 TGTTACAATG AAGAGGATGT CTATGTTTAT TTCACTTTTA TTAATGTACA ATAAATGTTC 1380
 TTGTTTCTTT AAAAAAAAAA AAAAAGTCGA G 1411

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Arg	Thr	Arg	Lys	Val	Asp	Ser	Leu	Leu	Leu	Leu	Ala	Ile	Pro	1	5	10	15
Gly	Leu	Ala	Leu	Leu	Leu	Leu	Pro	Asn	Ala	Tyr	Cys	Ala	Ser	Cys	Glu	20	25	30	
Pro	Val	Arg	Ile	Pro	Met	Cys	Lys	Ser	Met	Pro	Trp	Asn	Met	Thr	Lys	35	40	45	
Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	Ala	Ile	Leu	Ala	50	55	60	
Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Thr	Thr	Glu	Cys	Ser	Gln	Asp	Leu	65	70	75	80
Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	Thr	Ile	Asp	Phe	85	90	95	

Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val	Cys	Glu	Arg	Ala	Arg		
			100					105					110				
Ala	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg	His	Thr	Trp	Pro	Glu		
		115					120					125					
Ser	Leu	Ala	Cys	Glu	Glu	Leu	Pro	Val	Tyr	Asp	Arg	Gly	Val	Cys	Ile		
	130					135					140						
Ser	Pro	Glu	Ala	Ile	Val	Thr	Val	Glu	Gln	Gly	Thr	Asp	Ser	Met	Pro		
145					150					155					160		
Asp	Phe	Ser	Met	Asp	Ser	Asn	Asn	Gly	Asn	Cys	Gly	Ser	Gly	Arg	Glu		
				165					170					175			
His	Cys	Lys	Cys	Lys	Pro	Met	Lys	Ala	Thr	Gln	Lys	Thr	Tyr	Leu	Lys		
			180					185					190				
Asn	Asn	Tyr	Asn	Tyr	Val	Ile	Arg	Ala	Lys	Val	Lys	Glu	Val	Lys	Val		
		195					200					205					
Lys	Cys	His	Asp	Ala	Thr	Ala	Ile	Val	Glu	Val	Lys	Glu	Ile	Leu	Lys		
	210					215					220						
Ser	Ser	Leu	Val	Asn	Ile	Pro	Lys	Asp	Thr	Val	Thr	Leu	Tyr	Thr	Asn		
225					230					235					240		
Ser	Gly	Cys	Leu	Cys	Pro	Gln	Leu	Val	Ala	Asn	Glu	Glu	Tyr	Ile	Ile		
				245					250					255			
Met	Gly	Tyr	Glu	Asp	Lys	Glu	Arg	Thr	Arg	Leu	Leu	Leu	Val	Glu	Gly		
			260					265					270				
Ser	Leu	Ala	Glu	Lys	Trp	Arg	Asp	Arg	Leu	Ala	Lys	Lys	Val	Lys	Arg		
		275					280					285					
Trp	Asp	Gln	Lys	Leu	Arg	Arg	Pro	Arg	Lys	Ser	Lys	Asp	Pro	Val	Ala		
	290					295					300						
Pro	Ile	Pro	Asn	Lys	Asn	Ser	Asn	Ser	Arg	Gln	Ala	Arg	Ser				
305					310					315							

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTT TCACACAGGA CTCCTGGCAG AGGTGAATGG TTAGCCCTAT GGATTGTT	60
TGTTGATTTT GACACATGAT TGATTGCTTT CAGATAGGAT TGAAGGACTT GGATTTTAT	120
CTAATTCTGC ACTTTTAAAT TATCTGAGTA ATTGTTCATT TTGTATTGGA TGGGACTAAA	180
GATAAACTTA ACTCCTTGCT TTTGACTTGC CCATAAACTA TAAGGTGGGG TGAGTTGTAG	240
TTGCTTTTAC ATGTGCCCAG ATTTTCCCTG TATTCCCTGT ATTCCCTCTA AAGTAAGCCT	300
ACACATACAG GTTGGGCAGA ATAACAATGT CTCGAACAAG GAAAGTGGAC TCATTACTGC	360
TACTGGCCAT ACCTGGACTG GCGCTTCTCT TATTACCCAA TGCTTACTGT GCTTCGTGTG	420
AGCCTGTGCG GATCCCCATG TGCAAATCTA TGCCATGGAA CATGACCAAG ATGCCCAACC	480
ATCTCCACCA CAGCACTCAA GCCAATGCCA TCCTGGCAAT TGAACAGTTT GAAGGTTTGC	540
TGACCACTGA ATGTAGCCAG GACCTTTTGT TCTTTCTGTG TGCCATGTAT GCCCCATTT	600
GTACCATCGA TTTCCAGCAT GAACCAATTA AGCCTTGCAA GTCCGTGTGC GAAAGGGCCA	660
GGGCCGGCTG TGAGCCCATT CTCATAAAGT ACCGGCACAC TTGGCCAGAG AGCCTGGCAT	720
GTGAAGAGCT GCGCGTATAT GACAGAGGAG TCTGCATCTC CCCAGAGGCT ATCGTCACAG	780
TGGAACAAGG AACAGATTCA ATGCCAGACT TCTCCATGGA TTCAAACAAT GGAAATTGCG	840
GAAGCGGCAG GGAGCACTGT AAATGCAAGC CCATGAAGGC AACCCTAAAAG ACGTATCTCA	900
AGAATAATTA CAATTATGTA ATCAGAGCAA AAGTGAAAGA GGTGAAAGTG AAATGCCACG	960
ACGCAACAGC AATTGTGGAA GTAAAGGAGA TTCTCAAGTC TTCCCTAGTG AACATTCTTA	1020
AAGACACAGT GACACTGTAC ACCAACTCAG GCTGCTTGTTG CCCCAGCTT GTTGCCAATG	1080
AGGAATACAT AATTATGGGC TATGAAGACA AAGAGCGTAC CAGGCTTCTA CTAGTGAAG	1140
GATCCTTGGC CGAAAAATGG AGAGATCGTC TTGCTAAGAA AGTCAAGCGC TGGGATCAAA	1200
AGCTTCGACG TCCCAGGAAA AGCAAAGACC CCGTGGCTCC AATTCCCAAC AAAACAGCA	1260
ATTCCAGACA AGCGCGTAGT TAGACTAACG GAAAGGTGTA TGGAACTCT ATGGACTTTG	1320
AAACTAAGAT TTGCATTGTT GGAAGAGCAA AAAAGAAATT GCACTACAGC ACGTTATATT	1380
CTATTGTTTA CTACAAGAAG CTGGTTTAGT TGATTGTAGT TCTCCTTTCC TTCTTTTTTT	1440

TTATAACTAT ATTTGCACGT GTTCCCAGGC AATTGTTTTA TTCAACTTCC AGTGACAGAG	1500
CAGTGACTGA ATGTCTCAGC CTAAAGAAGC TCAATTCATT TCTGATCAAC TAATGGTGAC	1560
AAGTGTTTGA TACTTGGGGA AAGTGAAC TAATGCAATGG TAAATCAGAG AAAAGTTGAC	1620
CAATGTTGCT TTTCTGTAG ATGAACAAGT GAGAGATCAC ATTTAAATGA TGATCACTTT	1680
CCATTTAATA CTTTCAGCAG TTTTAGTTAG ATGACATGTA GGATGCACCT AAATCTAAAT	1740
ATTTTATCAT AAATGAAGAG CTGGTTTAGA CTGTATGGTC ACTGTTGGGA AGGTAAATGC	1800
CTACTTTGTC AATTCTGTTT TAAAAATTGC CTAAATAAAT ATTAAGTCCT AAATAAAAAA	1860
AAAAAAAAAA AAAAA	1875

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Leu	Leu	Leu	Phe	Arg	Ala	Ile	Pro	Met	Leu	Leu	Leu	Gly	Leu	Met	1	5	10	15
Val	Leu	Gln	Thr	Asp	Cys	Glu	Ile	Ala	Gln	Tyr	Tyr	Ile	Asp	Glu	Glu	20	25	30	
Glu	Pro	Pro	Gly	Thr	Val	Ile	Ala	Val	Leu	Ser	Gln	His	Ser	Ile	Phe	35	40	45	
Asn	Thr	Thr	Asp	Ile	Pro	Ala	Thr	Asn	Phe	Arg	Leu	Met	Lys	Gln	Phe	50	55	60	
Asn	Asn	Ser	Leu	Ile	Gly	Val	Arg	Glu	Ser	Asp	Gly	Gln	Leu	Ser	Ile	65	70	75	80
Met	Glu	Arg	Ile	Asp	Arg	Glu	Gln	Ile	Cys	Arg	Gln	Ser	Leu	His	Cys	85	90	95	
Asn	Leu	Ala	Leu	Asp	Val	Val	Ser	Phe	Ser	Lys	Gly	His	Phe	Lys	Leu	100	105	110	

Leu	Asn	Val	Lys	Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	His	Ser	Pro	His
	115						120					125			
Phe	Pro	Ser	Glu	Ile	Met	His	Val	Glu	Val	Ser	Glu	Ser	Ser	Ser	Val
	130					135					140				
Gly	Thr	Arg	Ile	Pro	Leu	Glu	Ile	Ala	Ile	Asp	Glu	Asp	Val	Gly	Ser
145					150					155					160
Asn	Ser	Ile	Gln	Asn	Phe	Gln	Ile	Ser	Asn	Asn	Ser	His	Phe	Ser	Ile
				165					170					175	
Asp	Val	Leu	Thr	Arg	Ala	Asp	Gly	Val	Lys	Tyr	Ala	Asp	Leu	Val	Leu
			180					185					190		
Met	Arg	Glu	Leu	Asp	Arg	Glu	Ile	Gln	Pro	Thr	Tyr	Ile	Met	Glu	Leu
		195					200					205			
Leu	Ala	Met	Asp	Gly	Gly	Val	Pro	Ser	Leu	Ser	Gly	Thr	Ala	Val	Val
	210					215					220				
Asn	Ile	Arg	Val	Leu	Asp	Phe	Asn	Asp	Asn	Ser	Pro	Val	Phe	Glu	Arg
225					230					235					240
Ser	Thr	Ile	Ala	Val	Asp	Leu	Val	Glu	Asp	Ala	Pro	Leu	Gly	Tyr	Leu
				245					250					255	
Leu	Leu	Glu	Leu	His	Ala	Thr	Asp	Asp	Asp	Glu	Gly	Val	Asn	Gly	Glu
			260					265					270		
Ile	Val	Tyr	Gly	Phe	Ser	Thr	Leu	Ala	Ser	Gln	Glu	Val	Arg	Gln	Leu
		275					280					285			
Phe	Lys	Ile	Asn	Ser	Arg	Thr	Gly	Ser	Val	Thr	Leu	Glu	Gly	Gln	Val
	290					295					300				
Asp	Phe	Glu	Thr	Lys	Gln	Thr	Tyr	Glu	Phe	Glu	Val	Gln	Ala	Gln	Asp
305					310					315					320
Leu	Gly	Pro	Asn	Pro	Leu	Thr	Ala	Thr	Cys	Lys	Val	Thr	Val	His	Ile
				325					330					335	
Leu	Asp	Val	Asn	Asp	Asn	Thr	Pro	Ala	Ile	Thr	Ile	Thr	Pro	Leu	Thr
			340					345					350		
Thr	Val	Asn	Ala	Gly	Val	Ala	Tyr	Ile	Pro	Glu	Thr	Ala	Thr	Lys	Glu
		355					360					365			
Asn	Phe	Ile	Ala	Leu	Ile	Ser	Thr	Thr	Asp	Arg	Ala	Ser	Gly	Ser	Asn
	370					375					380				

Gly	Gln	Val	Arg	Cys	Thr	Leu	Tyr	Gly	His	Glu	His	Phe	Lys	Leu	Gln	385	390	395	400
Gln	Ala	Tyr	Glu	Asp	Ser	Tyr	Met	Ile	Val	Thr	Thr	Ser	Thr	Leu	Asp	405	410	415	
Arg	Glu	Asn	Ile	Ala	Ala	Tyr	Ser	Leu	Thr	Val	Val	Ala	Glu	Asp	Leu	420	425	430	
Gly	Phe	Pro	Ser	Leu	Lys	Thr	Lys	Lys	Tyr	Tyr	Thr	Val	Lys	Val	Ser	435	440	445	
Asp	Glu	Asn	Asp	Asn	Ala	Pro	Val	Phe	Ser	Lys	Pro	Gln	Tyr	Glu	Ala	450	455	460	
Ser	Ile	Leu	Glu	Asn	Asn	Ala	Pro	Gly	Ser	Tyr	Ile	Thr	Thr	Val	Ile	465	470	475	480
Ala	Arg	Asp	Ser	Asp	Ser	Asp	Gln	Asn	Gly	Lys	Val	Asn	Tyr	Arg	Leu	485	490	495	
Val	Asp	Ala	Lys	Val	Met	Gly	Gln	Ser	Leu	Thr	Thr	Phe	Val	Ser	Leu	500	505	510	
Asp	Ala	Asp	Ser	Gly	Val	Leu	Arg	Ala	Val	Arg	Ser	Leu	Asp	Tyr	Glu	515	520	525	
Lys	Leu	Lys	Gln	Leu	Asp	Phe	Glu	Ile	Glu	Ala	Ala	Asp	Asn	Gly	Ile	530	535	540	
Pro	Gln	Leu	Ser	Thr	Arg	Val	Gln	Leu	Asn	Leu	Arg	Ile	Val	Asp	Gln	545	550	555	560
Asn	Asp	Asn	Cys	Pro	Val	Ile	Thr	Asn	Pro	Leu	Leu	Asn	Asn	Gly	Ser	565	570	575	
Gly	Glu	Val	Leu	Leu	Pro	Ile	Ser	Ala	Pro	Gln	Asn	Tyr	Leu	Val	Phe	580	585	590	
Gln	Leu	Lys	Ala	Glu	Asp	Ser	Asp	Glu	Gly	His	Asn	Ser	Gln	Leu	Phe	595	600	605	
Tyr	Thr	Ile	Leu	Arg	Asp	Pro	Ser	Arg	Leu	Phe	Ala	Ile	Asn	Lys	Glu	610	615	620	
Ser	Gly	Glu	Val	Phe	Leu	Lys	Lys	Gln	Leu	Asn	Ser	Asp	His	Ser	Glu	625	630	635	640
Asp	Leu	Ser	Ile	Val	Val	Ala	Val	Tyr	Asp	Leu	Gly	Arg	Pro	Ser	Leu	645	650	655	

Ser	Thr	Asn	Ala	Thr	Val	Lys	Phe	Ile	Leu	Thr	Asp	Ser	Phe	Pro	Ser		
			660					665					670				
Asn	Val	Glu	Val	Val	Ile	Leu	Gln	Pro	Ser	Ala	Glu	Glu	Gln	His	Gln		
		675					680					685					
Ile	Asp	Met	Ser	Ile	Ile	Phe	Ile	Ala	Val	Leu	Ala	Gly	Gly	Cys	Ala		
	690					695					700						
Leu	Leu	Leu	Leu	Ala	Ile	Phe	Phe	Val	Ala	Cys	Thr	Cys	Lys	Lys	Lys		
705					710					715					720		
Ala	Gly	Glu	Phe	Lys	Gln	Val	Pro	Glu	Gln	His	Gly	Thr	Cys	Asn	Glu		
				725					730					735			
Glu	Arg	Leu	Leu	Ser	Thr	Pro	Ser	Pro	Gln	Ser	Val	Ser	Ser	Ser	Leu		
		740						745					750				
Ser	Gln	Ser	Glu	Ser	Cys	Gln	Leu	Ser	Ile	Asn	Thr	Glu	Ser	Glu	Asn		
		755					760					765					
Cys	Ser	Val	Ser	Ser	Asn	Gln	Glu	Gln	His	Gln	Gln	Thr	Gly	Ile	Lys		
	770					775					780						
His	Ser	Ile	Ser	Val	Pro	Ser	Tyr	His	Thr	Ser	Gly	Trp	His	Leu	Asp		
785					790					795					800		
Asn	Cys	Ala	Met	Ser	Ile	Ser	Gly	His	Ser	His	Met	Gly	His	Ile	Ser		
				805					810					815			
Thr	Lys	Asp	Ser	Gly	Lys	Gly	Asp	Ser	Asp	Phe	Asn	Asp	Ser	Asp	Ser		
			820					825						830			
Asp	Thr	Ser	Gly	Glu	Ser	Gln	Lys	Lys	Ser	Ile	Glu	Gln	Pro	Met	Gln		
		835					840					845					
Ala	Gln	Ala	Ser	Ala	Gln	Tyr	Thr	Asp	Glu	Ser	Ala	Gly	Phe	Arg	His		
	850					855					860						
Ala	Asp	Asn	Tyr	Phe	Ser	His	Arg	Ile	Asn	Lys	Gly	Pro	Glu	Asn	Gly		
865					870					875					880		
Asn	Cys	Thr	Leu	Gln	Tyr	Glu	Lys	Gly	Tyr	Arg	Leu	Ser	Tyr	Ser	Val		
				885					890					895			
Ala	Pro	Ala	His	Tyr	Asn	Thr	Tyr	His	Ala	Arg	Met	Pro	Asn	Leu	His		
			900					905					910				
Ile	Pro	Asn	His	Thr	Leu	Arg	Asp	Pro	Tyr	Tyr	His	Ile	Asn	Asn	Pro		
		915					920					925					

Val Ala Asn Arg Met His Ala Glu Tyr Glu Arg Asp Leu Val Asn Arg
930 935 940

Ser Ala Thr Leu Ser Pro Gln Arg Ser Ser Ser Arg Tyr Gln Glu Phe
945 950 955 960

Asn Tyr Ser Pro Gln Ile Ser Arg Gln Leu His Pro Ser Glu Ile Ala
965 970 975

Thr Thr Phe

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3655 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCCAG AGATGAACTC CTTGAGATTG TTTTAAATGA CTGCAGGTCT GGAAGGATTC	60
ACATTGCCAC ACTGTTTCTA GGCATGAAAA AACTGCAAGT TTCAACTTTG TTTTGGGTGC	120
AACTTTGATT CTTCAAGATG CTGCTTCTCT TCAGAGCCAT TCCAATGCTG CTGTTGGGAC	180
TGATGGTTTT ACAAACAGAC TGTGAAATTG CCCAGTACTA CATAGATGAA GAAGAACCCC	240
CTGGCACTGT AATTGCAGTG TTGTCACAAC ACTCCATATT TAACACTACA GATATACCTG	300
CAACCAATTT CCGTCTAATG AAGCAATTTA ATAATTCCTT TATCGGAGTC CGTGAGAGTG	360
ATGGGCAGCT GAGCATCATG GAGAGGATTG ACCGGGAGCA AATCTGCAGG CAGTCCCTTC	420
ACTGCAACCT GGCTTTGGAT GTGGTCAGCT TTTCCAAAGG ACACTTCAAG CTTCTGAACG	480
TGAAAGTGGA GGTGAGAGAC ATTAATGACC ATAGCCCTCA CTTTCCCAGT GAAATAATGC	540
ATGTGGAGGT GTCTGAAAGT TCCTCTGTGG GCACCAGGAT TCCTTTAGAA ATTGCAATAG	600
ATGAAGATGT TGGGTCCAAC TCCATCCAGA ACTTTCAGAT CTCAAATAAT AGCCACTTCA	660
GCATTGATGT GCTAACCAGA GCAGATGGGG TGAAATATGC AGATTTAGTC TTAATGAGAG	720
AACTGGACAG GGAAATCCAG CCAACATACA TAATGGAGCT ACTAGCAATG GATGGGGGTG	780

TACCATCACT	ATCTGGTACT	GCAGTGGTTA	ACATCCGAGT	CCTGGACTTT	AATGATAACA	840
GCCCAGTGTT	TGAGAGAAGC	ACCATTGCTG	TGGACCTAGT	AGAGGATGCT	CCTCTGGGAT	900
ACCTTTTGTT	GGAGTTACAT	GCTACTGACG	ATGATGAAGG	AGTGAATGGA	GAAATTGTTT	960
ATGGATTGAG	CACTTTGGCA	TCTCAAGAGG	TACGTCAGCT	ATTTAAAATT	AACTCCAGAA	1020
CTGGCAGTGT	TACTCTTGAA	GGCCAAGTTG	ATTTTGAGAC	CAAGCAGACT	TACGAATTTG	1080
AGGTACAAGC	CCAAGATTTG	GGCCCCAACC	CACTGACTGC	TACTTGTAAG	GTAAGTGTTC	1140
ATATACTTGA	TGTAAATGAT	AATACCCAG	CCATCACTAT	TACCCCTCTG	ACTACTGTAA	1200
ATGCAGGAGT	TGCCTATATT	CCAGAAACAG	CCACAAAGGA	GAAGTTTATA	GCTCTGATCA	1260
GCACTACTGA	CAGAGCCTCT	GGATCTAATG	GACAAGTTCG	CTGTACTCTT	TATGGACATG	1320
AGCACTTTAA	ACTACAGCAA	GCTTATGAGG	ACAGTTACAT	GATAGTTACC	ACCTCTACTT	1380
TAGACAGGGA	AAACATAGCA	GCGTACTCTT	TGACAGTAGT	TGCAGAAGAC	CTTGGCTTCC	1440
CCTCATTGAA	GACCAAAAAG	TACTACACAG	TCAAGGTTAG	TGATGAGAAT	GACAATGCAC	1500
CTGTATTTTC	TAAACCCAG	TATGAAGCTT	CTATTCTGGA	AAATAATGCT	CCAGGCTCTT	1560
ATATACTAC	AGTGATAGCC	AGAGACTCTG	ATAGTGATCA	AAATGGCAA	GTAAATTACA	1620
GACTTGTGGA	TGCAAAAGTG	ATGGGCCAGT	CACTAACAAC	ATTTGTTTCT	CTTGATGCGG	1680
ACTCTGGAGT	ATTGAGAGCT	GTTAGGTCTT	TAGACTATGA	AAACTTAAA	CACTGGATT	1740
TTGAAATTGA	AGCTGCAGAC	AATGGGATCC	CTCAACTCTC	CACTCGCGTT	CACTAAATC	1800
TCAGAATAGT	TGATCAAAAT	GATAATTGCC	CTGTGATAAC	TAATCCTCTT	CTTAATAATG	1860
GCTCGGGTGA	AGTTCTGCTT	CCCATCAGCG	CTCCTCAAAA	CTATTTAGTT	TTCCAGCTCA	1920
AAGCCGAGGA	TTCAGATGAA	GGGCACAACT	CCCAGCTGTT	CTATACCATA	CTGAGAGATC	1980
CAAGCAGATT	GTTTGCCATT	AACAAAGAAA	GTGGTGAAGT	GTTTCTGAAA	AAACAATTAA	2040
ACTCTGACCA	TTCAGAGGAC	TTGAGCATAG	TAGTTGCAGT	GTATGACTTG	GGAAGACCTT	2100
CATTATCCAC	CAATGCTACA	GTTAAATTCA	TCCTCACCAG	CTCTTTTCCT	TCTAACGTTG	2160
AAGTCGTTAT	TTTGCAACCA	TCTGCAGAAG	AGCAGCACCA	GATCGATATG	TCCATTATAT	2220
TCATTGCAGT	GCTGGCTGGT	GGTGTGCTT	TGCTACTTTT	GGCCATCTTT	TTTGTGGCCT	2280
GTAAGTGTAA	AAAGAAAGCT	GGTGAATTTA	AGCAGGTACC	TGAACAACAT	GGAACATGCA	2340

ATGAAGAACG CCTGTTAAGC ACCCCATCTC CCCAGTCGGT CTCTTCTTCT TTGTCTCAGT	2400
CTGAGTCATG CCAACTCTCC ATCAATACTG AATCTGAGAA TTGCAGCGTG TCCTCTAACC	2460
AAGAGCAGCA TCAGCAAACA GGCATAAAGC ACTCCATCTC TGTACCATCT TATCACACAT	2520
CTGGTTGGCA CCTGGACAAT TGTGCAATGA GCATAAGTGG ACATTCTCAC ATGGGGCACA	2580
TTAGTACAAA GGACAGTGGC AAAGGAGATA GTGACTTCAA TGACAGTGAC TCTGATACTA	2640
GTGGAGAATC ACAAAGAAG AGCATTGAGC AGCCAATGCA GGCACAAGCC AGTGCTCAAT	2700
ACACAGATGA ATCAGCAGGG TTCCGACATG CCGATAACTA TTTCAGCCAC CGAATCAACA	2760
AGGGTCCAGA AAATGGGAAC TGCACATTGC AATATGAAAA GGGCTATAGA CTGTCTTACT	2820
CTGTAGCTCC TGCTCATTAC AATACCTACC ATGCAAGAAT GCCTAACCTG CACATACCGA	2880
ACCATACCCT TAGAGACCCT TATTACCATA TCAATAATCC TGTTGCTAAT CGGATGCACG	2940
CGGAATATGA AAGAGATTTA GTCAACAGAA GTGCAACGTT ATCTCCGCAG AGATCGTCTA	3000
GCAGATACCA AGAATTCAAT TACAGTCCGC AGATATCAAG ACAGCTTCAT CCTTCAGAAA	3060
TTGCTACAAC CTTTTAATCA TTAGGCATGC AAGTGAGAAT GCACAAAGGC AAGTGCTTTA	3120
GCATGAAAGC TAAATATATG GAGTCTCCCC TTTCCCTCTG ATGGATGGGG GGAGACACAG	3180
GACAGTGCAT AAATATACAG CTGCTTTCTA TTTGCATTTT ACTTGGAAT TTTTTGTTTT	3240
TTTTACATAT TTATTTTCC TGAATTGAAT GTGACATTGT CCTGTCACCT AACTAGCAAT	3300
TAAATCCACA GACCTACAGT CAAATATTTG AGGGCCCCTG AAACAGCACA TCAGTCAGGA	3360
CCTAAAGTGG CCTTTTTACT TTTAGCAGCT CCTGGGTCTG CCCTCTGTGT TAATCAGCCC	3420
CTGGTCAAGT CCTGAGTAGG ATCATGGCGT TTTTATATGC ATCTCACCTA CTTTGGACGT	3480
GATTTACACA TAATAGGAAA CGCTTGGTTT CAGTGAAGTC TGTGTTGTAT ATATTCTGTT	3540
ATATACACGC ATTTTGTGTT TGTGTATATA TTTCAAGTCC ATTCAGATAT GTGTATATAG	3600
TGCAGACCTT GTAAATTAAA TATTCTGATA CTTTTTCCTC AATAAATATT TAAAT	3655

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Val	Cys	Cys	Gly	Pro	Gly	Arg	Met	Leu	Leu	Gly	Trp	Ala	Gly	Leu	
1				5					10					15		
Leu	Val	Leu	Ala	Ala	Leu	Cys	Leu	Leu	Gln	Val	Pro	Gly	Ala	Gln	Ala	
			20					25					30			
Ala	Ala	Cys	Glu	Pro	Val	Arg	Ile	Pro	Leu	Cys	Lys	Ser	Leu	Pro	Trp	
		35					40					45				
Asn	Met	Thr	Lys	Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	
	50					55					60					
Ala	Ile	Leu	Ala	Met	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Gly	Thr	His	Cys	
65					70					75					80	
Ser	Pro	Asp	Leu	Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	
			85						90					95		
Thr	Ile	Asp	Phe	Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val	Cys	
			100					105					110			
Glu	Arg	Ala	Arg	Gln	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg	His	
		115					120					125				
Ser	Trp	Pro	Glu	Ser	Leu	Ala	Cys	Asp	Glu	Leu	Pro	Val	Tyr	Asp	Arg	
	130					135					140					
Gly	Val	Cys	Ile	Ser	Pro	Glu	Ala	Ile	Val	Thr	Ala	Asp	Gly	Ala	Asp	
145					150					155					160	
Phe	Pro	Met	Asp	Ser	Ser	Thr	Gly	His	Cys	Arg	Gly	Ala	Ser	Ser	Glu	
				165					170					175		
Arg	Cys	Lys	Cys	Lys	Pro	Val	Arg	Ala	Thr	Gln	Lys	Thr	Tyr	Phe	Arg	
			180					185					190			
Asn	Asn	Tyr	Asn	Tyr	Val	Ile	Arg	Ala	Lys	Val	Lys	Glu	Val	Lys	Met	
		195					200					205				
Lys	Cys	His	Asp	Val	Thr	Ala	Val	Val	Glu	Val	Lys	Glu	Ile	Leu	Lys	
	210					215					220					
Ala	Ser	Leu	Val	Asn	Ile	Pro	Arg	Asp	Thr	Val	Asn	Leu	Tyr	Thr	Thr	
225					230					235					240	

Ser Gly Cys Leu Cys Pro Pro Leu Thr Val Asn Glu Glu Tyr Val Ile
 245 250 255
 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Met Lys Leu Arg His Leu Gly Leu Gly Lys Thr Asp Ala Ser
 290 295 300
 Asp Ser Thr Gln Asn Gln Lys Ser Gly Arg Asn Ser Asn Pro Arg Pro
 305 310 315 320
 Ala Arg Ser

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCCTGGGA CCATGGTCTG CTGCGGCCCG GGACGGATGC TGCTAGGATG GGCCGGGTTG	60
CTAGTCCTGG CTGCTCTCTG CCTGCTCCAG GTGCCCGGAG CTCAGGCTGC AGCCTGTGAG	120
CCTGTCCGCA TCCCGCTGTG CAAGTCCCTT CCCTGGAACA TGACCAAGAT GCCCAACCAC	180
CTGCACCACA GCACCCAGGC TAACGCCATC CTGGCCATGG AACAGTTCGA AGGGCTGCTG	240
GGCACCCACT GCAGCCCGGA TCTTCTCTTC TTCCTCTGTG CAATGTACGC ACCCATTTGC	300
ACCATCGACT TCCAGCACGA GCCCATCAAG CCCTGCAAGT CTGTGTGTGA GCGCGCCCGA	360
CAGGGCTGCG AGCCCATTTCT CATCAAGTAC CGCCACTCGT GGCCGGAAAG CTTGGCCTGC	420
GACGAGCTGC CGGTGTACGA CCGCGGCGTG TGCATCTCTC CTGAGGCCAT CGTCACCGCG	480
GACGGAGCGG ATTTTCCTAT GGATTCAAGT ACTGGACACT GCAGAGGGGC AAGCAGCGAA	540
CGTTGCAAAT GTAAGCCTGT CAGAGCTACA CAGAAGACCT ATTTCCGGAA CAATTACAAC	600

TATGTCATCC	GGGCTAAAGT	TAAAGAGGTA	AAGATGAAAT	GTCATGATGT	GACCGCCGTT	660
GTGGAAGTGA	AGGAAATTCT	AAAGGCATCA	CTGGTAAACA	TTCCAAGGGA	CACCGTCAAT	720
CTTTATACCA	CCTCTGGCTG	CCTCTGTCCT	CCACTTACTG	TCAATGAGGA	ATATGTCATC	780
ATGGGCTATG	AAGACGAGGA	ACGTTCCAGG	TTACTCTTGG	TAGAAGGCTC	TATAGCTGAG	840
AAGTGGAAGG	ATCGGCTTGG	TAAGAAAGTC	AAGCGCTGGG	ATATGAAACT	CCGACACCTT	900
GGACTGGGTA	AAACTGATGC	TAGCGATTCC	ACTCAGAATC	AGAAGTCTGG	CAGGAACTCT	960
AATCCCCGGC	CAGCACGCAG	CTAAATCCTG	AAATGTAAAA	GGCCACACCC	ACGGACTCCC	1020
TTCTAAGACT	GGCGCTGGTG	GACTAACAAA	GGAAAACCGC	ACAGTTGTGC	TCGTGACCGA	1080
TTGTTTACCG	CAGACACCGC	GTGGCTACCG	AAGTTACTTC	CGGTCCCCTT	TCTCCTGCTT	1140
CTTAATGGCG	TGGGGTTAGA	TCCTTTAATA	TGTTATATAT	TCTGTTTCAT	CAATCACGTG	1200
GGGACTGTTC	TTTTGCAACC	AGAATAGTAA	ATTAAATATG	TTGATGCTAA	GGTTTCTGTA	1260
CTGGACTCCC	TGGGTTTAAT	TTGGTGTTCT	GTACCCTGAT	TGAGAATGCA	ATGTTTCATG	1320
TAAAGAGAGA	ATCCTGGTCA	TATCTCAAGA	ACTAGATATT	GCTGTAAGAC	AGCCTCTGCT	1380
GCTGCGCTTA	TAGTCTTGTG	TTTGTATGCC	TTTGTCCATT	TCCCTCATGC	TGTGAAAGTT	1440
ATACATGTTT	ATAAAGGTAG	AACGGCATTT	TGAAATCAGA	CACTGCACAA	GCAGAGTAGC	1500
CCAACACCAG	GAAGCATTTA	TGAGGAAACG	CCACACAGCA	TGACTTATTT	TCAAGATTGG	1560
CAGGCAGCAA	AATAAATAGT	GTTGGGAGCC	AAGAAAAGAA	TATTTTGCCT	GGTTAAGGGG	1620
CACACTGGAA	TCAGTAGCCC	TTGAGCCATT	AACAGCAGTG	TTCTTCTGGC	AAGTTTTTGA	1680
TTTGTTTATA	AATGTATTCA	CGAGCATTAG	AGATGAACTT	ATAACTAGAC	ATCTGTTGTT	1740
ATCTCTATAG	CTCTGCTTCC	TTCTAAATCA	AACCCATTGT	TGGATGCTCC	CTCTCCATTC	1800
ATAAATAAAT	TTGGCTTGCT	GTATTGGCCA	GGAAAAGAAA	GTATTAAAGT	ATGCATGCAT	1860
GTGCACCAGG	GTGTTATTTA	ACAGAGGTAT	GTAACCTCTAT	AAAAGACTAT	AATTTACAGG	1920
ACACGGAAAT	GTGCACATTT	GTTTACTTTT	TTTCTTCCTT	TTGCTTTGGG	CTTGTGATTT	1980
TGGTTTTTTG	TGTGTTTATG	TCTGTATTTT	GGGGGGTGGG	TAGGTTTAAG	CCATTGCACA	2040
TTCAAGTTGA	ACTAGATTAG	AGTAGACTAG	GCTCATTGGC	CTAGACATTA	TGATTTGAAT	2100

TTGTGTTGTT TAATGCTCCA TCAAGATGTC TAATAAAAGG AATATGGTTG TCAACAGAGA 2160
CGACAACAAC AACAAA 2176

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Val	Cys	Gly	Ser	Pro	Gly	Gly	Met	Leu	Leu	Leu	Arg	Ala	Gly	Leu	1	5	10	15
Leu	Ala	Leu	Ala	Ala	Leu	Cys	Leu	Leu	Arg	Val	Pro	Gly	Ala	Arg	Ala	20	25	30	
Ala	Ala	Cys	Glu	Pro	Val	Arg	Ile	Pro	Leu	Cys	Lys	Ser	Leu	Pro	Trp	35	40	45	
Asn	Met	Thr	Lys	Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	50	55	60	
Ala	Ile	Leu	Ala	Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Gly	Thr	His	Cys	65	70	75	80
Ser	Pro	Asp	Leu	Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	85	90	95	
Thr	Ile	Asp	Phe	Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val	Cys	100	105	110	
Glu	Arg	Ala	Arg	Gln	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg	His	115	120	125	
Ser	Trp	Pro	Glu	Asn	Leu	Ala	Cys	Glu	Glu	Leu	Pro	Val	Tyr	Asp	Arg	130	135	140	
Gly	Val	Cys	Ile	Ser	Pro	Glu	Ala	Ile	Val	Thr	Ala	Asp	Gly	Ala	Asp	145	150	155	160
Phe	Pro	Met	Asp	Ser	Ser	Asn	Gly	Asn	Cys	Arg	Gly	Ala	Ser	Ser	Glu	165	170	175	

Arg	Cys	Lys	Cys	Lys	Pro	Ile	Arg	Ala	Thr	Gln	Lys	Thr	Tyr	Phe	Arg	
			180					185					190			
Asn	Asn	Tyr	Asn	Tyr	Val	Ile	Arg	Ala	Lys	Val	Lys	Glu	Ile	Lys	Thr	
		195					200					205				
Lys	Cys	His	Asp	Val	Thr	Ala	Val	Val	Glu	Val	Lys	Glu	Ile	Leu	Lys	
	210					215					220					
Ser	Ser	Leu	Val	Asn	Ile	Pro	Arg	Asp	Thr	Val	Asn	Leu	Tyr	Thr	Ser	
225					230					235					240	
Ser	Gly	Cys	Leu	Cys	Pro	Pro	Leu	Asn	Val	Asn	Glu	Glu	Tyr	Ile	Ile	
				245					250					255		
Met	Gly	Tyr	Glu	Asp	Glu	Glu	Arg	Ser	Arg	Leu	Leu	Leu	Val	Glu	Gly	
			260					265					270			
Ser	Ile	Ala	Glu	Lys	Trp	Lys	Asp	Arg	Leu	Gly	Lys	Lys	Val	Lys	Arg	
		275					280					285				
Trp	Asp	Met	Lys	Leu	Arg	His	Leu	Gly	Leu	Ser	Lys	Ser	Asp	Ser	Ser	
	290					295					300					
Asn	Ser	Asp	Ser	Thr	Gln	Ser	Gln	Lys	Ser	Gly	Arg	Asn	Ser	Asn	Pro	
305					310					315					320	
Arg	Gln	Ala	Arg	Asn												
				325												

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1893 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCGGAGCGG	GCCTTTTGGC	GTCCACTGCG	CGGCTGCACC	CTGCCCCATC	TGCCGGGATC	60
ATGGTCTGCG	GCAGCCCGGG	AGGGATGCTG	CTGCTGCGGG	CCGGGCTGCT	TGCCCTGGCT	120
GCTCTCTGCC	TGCTCCGGGT	GCCCGGGGCT	CGGGCTGCAG	CCTGTGAGCC	CGTCCGCATC	180
CCCCTGTGCA	AGTCCCTGCC	CTGGAACATG	ACTAAGATGC	CCAACCACCT	GCACCACAGC	240

ACTCAGGCCA	ACGCCATCCT	GGCCATCGAG	CAGTTCGAAG	GTCTGCTGGG	CACCCACTGC	300
AGCCCCGATC	TGCTCTTCTT	CCTCTGTGCC	ATGTACGCGC	CCATCTGCAC	CATTGACTTC	360
CAGCACGAGC	CCATCAAGCC	CTGTAAGTCT	GTGTGCGAGC	GGGCCCCGGCA	GGGCTGTGAG	420
CCCATACTCA	TCAAGTACCG	CCACTCGTGG	CCGGAGAACC	TGGCCTGCGA	GGAGCTGCCA	480
GTGTACGACA	GGGGCGTGTG	CATCTCTCCC	GAGGCCATCG	TTACTGCGGA	CGGAGCTGAT	540
TTTCCTATGG	ATTCTAGTAA	CGGAAACTGT	AGAGGGGCAA	GCAGTGAACG	CTGTAAATGT	600
AAGCCTATTA	GAGCTACACA	GAAGACCTAT	TTCCGGAACA	ATTACAATA	TGTCATTCCG	660
GCTAAAGTTA	AAGAGATAAA	GACTAAGTGC	CATGATGTGA	CTGCAGTAGT	GGAGGTGAAG	720
GAGATTCTAA	AGTCCTCTCT	GGTAAACATT	CCACGGGACA	CTGTCAACCT	CTATACCAGC	780
TCTGGCTGCC	TCTGCCCTCC	ACTTAATGTT	AATGAGGAAT	ATATCATCAT	GGGCTATGAA	840
GATGAGGAAC	GTTCCAGATT	ACTCTTGGTG	GAAGGCTCTA	TAGCTGAGAA	GTGGAAGGAT	900
CGACTCGGTA	AAAAAGTTAA	GCGCTGGGAT	ATGAAGCTTC	GTCATCTTGG	ACTCAGTAAA	960
AGTGATTCTA	GCAATAGTGA	TTCCACTCAG	AGTCAGAAGT	CTGGCAGGAA	CTCGAACCCC	1020
CGGCAAGCAC	GCAACTAAAT	CCCGAAATAC	AAAAAGTAAC	ACAGTGGACT	TCCTATTAAG	1080
ACTTACTTGC	ATTGCTGGAC	TAGCAAAGGA	AAATTGCACT	ATTGCACATC	ATATTCTATT	1140
GTTTACTATA	AAAATCATGT	GATAACTGAT	TATTACTTCT	GTTTCTCTTT	TGGTTTCTGC	1200
TTCTCTCTTC	TCTCAACCCC	TTTGTAATGG	TTTGGGGGCA	GACTCTTAAG	TATATTGTGA	1260
GTTTTCTATT	TCACTAATCA	TGAGAAAAAC	TGTTCTTTTG	CAATAATAAT	AAATTAAACA	1320
TGCTGTTACC	AGAGCCTCTT	TGCTGAGTCT	CCAGATGTTA	ATTTACTTTC	TGCACCCCAA	1380
TTGGGAATGC	AATATTGGAT	GAAAAGAGAG	GTTTCTGGTA	TTCACAGAAA	GCTAGATATG	1440
CCTTAAACA	TACTCTGCCG	ATCTAATTAC	AGCCTTATTT	TTGTATGCCT	TTTGGGCATT	1500
CTCCTCATGC	TTAGAAAGTT	CCAAATGTTT	ATAAAGGTAA	AATGGCAGTT	TGAAGTCAAA	1560
TGTCACATAG	GCAAAGCAAT	CAAGCACCAG	GAAGTGTTTA	TGAGGAAACA	ACACCCAAGA	1620
TGAATTATTT	TTGAGACTGT	CAGGAAGTAA	AATAAATAGG	AGCTTAAGAA	AGAACATTTT	1680
GCCTGATTGA	GAAGCACAAC	TGAAACCAGT	AGCCGCTGGG	GTGTTAATGG	TAGCATTCTT	1740
CTTTTGCAA	TACATTTGAT	TTGTTTCATGA	ATATATTAAT	CAGCATTAGA	GAAATGAATT	1800

ATAACTAGAC ATCTGCTGTT ATCACCATAG TTTGTTTAA TTTGCTTCCT TTAAATAAA 1860

CCCATTGGTG AAAGTCAAAA AAAAAAAAAA AAA 1893